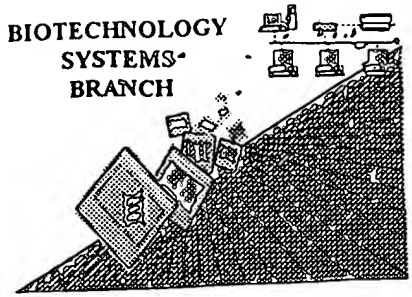


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/972916

Source: DFPE

Date Processed by STIC: 10/19/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/972916

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Does Not Comply
Corrected Diskette Needed

*
Does Not Comply
Corrected Diskette Needed

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Current Application date is 10-10-01
It is required that new format and
new rules are adhered to not a
mixture of both old and new format and
rules.

MA

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/972,916

DATE: 10/19/2001
TIME: 10:48:35

Input Set: I972916.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Thul, Peter M.
2 <120> TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
3 <130> FILE REFERENCE: US 1292/01 (VA)
4 <140> CURRENT APPLICATION NUMBER: US/09/972,916
5 <141> CURRENT FILING DATE: 2001-10-10
6 ~~<150> EARLIER APPLICATION NUMBER~~
7 <151> EARLIER FILING DATE: *These fields are mandatory if you wish to claim prior property right. mtd*
8 <160> NUMBER OF SEQ ID NOS: 6
9 <210> SEQ ID NO 1
10 <211> LENGTH: 51
11 <212> TYPE: DNA
12 <213> ORGANISM: Rattus norvegicus
13 <220> FEATURE:
14 <221> NAME/KEY:
15 <222> LOCATION:
16 <223> OTHER INFORMATION: STRANDEDNESS: double
17 TOPOLOGY: linear
18 <400> SEQUENCE: SEQ ID NO: 1
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20 <210> SEQ ID NO 2
21 <211> LENGTH: 219
22 <212> TYPE: DNA
23 <213> ORGANISM: Rattus norvegicus
24 <220> FEATURE:
25 <221> NAME/KEY:
26 <222> LOCATION:
27 <223> OTHER INFORMATION: STRANDEDNESS: double
28 TOPOLOGY: linear
29 <400> SEQUENCE: SEQ ID NO: 2
30 tcacaagcaa aacaaactta ttttgaacac ggggataccta gcacgctgcc ctgacaatca 60
31 ttaaccctgt ctgccgagcc agcccttcat aaggccctgg gtatggccag ccagcatggt 120
32 ccactgcccg ccgagacaca aaccagcgca gcattgaaca ctgcacacgg ccactctgcc 180
33 agagagctgt gaccaccact tccgtacta gctagccgc 219
34 <210> SEQ ID NO 3
35 <211> LENGTH: 270
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <221> NAME/KEY:
40 <222> LOCATION:
41 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
42 STRANDEDNESS: double
43 TOPOLOGY: both
44 <400> SEQUENCE: SEQ ID NO: 3

OR If you wish to use old Format. Does Not Comply Corrected Diskette Needed mtd

Does Not Comply Corrected Diskette Needed

Errored

choose new format

Errored

W-->

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/972,916

DATE: 10/19/2001
TIME: 10:48:35

Input Set: I972916.RAW

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45      catgggcgca cggggcactc ccgtggttcc tggactctgg cccccagtgt atcacaagca      60
46      aaacaaactt attttgaaca cggggatcct agcacgctgc cctgacaatc attaaccctg      120
47      gctgccgagc cagcccttca taaggccctg ggtatggcca gccagcatgg tccactgccc      180
48      gccgagacac aaaccagcg agcattgaac actgcacacg gccatctgcc cagagagctg      240
49      tgaccaccac ttccgctact agctagccgc                                270

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50 <210> SEQ ID NO 4
51 <211> LENGTH: 321
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <221> NAME/KEY:
56 <222> LOCATION:
57 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
58     STRANDEDNESS: double
59     TOPOLOGY: both

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60 <400> SEQUENCE: SEQ ID NO: 4
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62      ggccagagtc caggaaccac gggagtgtccc cgtgcgcccac tgcacaagc aaaacaaact      120
63      tattttgaac acggggatcc tagcacgctg ccctgacaat cattaaccctg tgctgccgag      180
64      ccagcccttc ataaggccct gggatgtggc agccagcatg gtccactgcc cgccgagaca      240
65      caaaccagc gagcattgaa cactgcacac ggccatctgc ccagagagct gtgaccacca      300
66      cttccgctac tagctagccg c                                321

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67 <210> SEQ ID NO 5
68 <211> LENGTH: 372
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <221> NAME/KEY:
73 <222> LOCATION:
74 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
75     STRANDEDNESS: double
76     TOPOLOGY: both

```

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77 <400> SEQUENCE: SEQ ID NO: 5
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79      ggccagagtc caggaaccac gggagtgtccc cgtgcgcccac tgcactgg gggccagagt      120
80      ccaggaacca cgggagtgtc ccgtgcgccc atgtcacaag caaaacaaac ttattttgaa      180
81      cacggggatc ctagcacgct gccctgacaa tcattaacct gtgctgccga gccagccctt      240
82      cataaggccc tgggtatggc cagccagcat ggtccactgc ccgccgagac acaaacccag      300
83      cgagcattga aactgcaca cgccatctg cccagagagc tgtgaccacc acttccgcta      360
84      ctagctagcc gc                                372

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85 <210> SEQ ID NO 6
86 <211> LENGTH: 423
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <221> NAME/KEY:
91 <222> LOCATION:
92 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
93     STRANDEDNESS: double
94     TOPOLOGY: both

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Errored

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/972,916DATE: 10/19/2001
TIME: 10:48:35

Input Set: I972916.RAW

95 <400> SEQUENCE: SEQ ID NO: 6
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97 acggggcact cccgtgggtc ctggactctg gccccagtg tacatgggcg cacggggcac 120
98 tcccgtggtt cctggactct ggccccaggt gtacatgggc gcacggggca ctcccgtggt 180
99 tcctggactc tggccccagc tgtatcaca gcaaaacaaa cttattttga acacggggat 240
100 cctagcacgc tgccctgaca atcattaacc cgtgctgccg agccagccct tcataaggcc 300
101 ctgggtatgg ccagccagca tgggccactg cccgccgaga cacaaaccca gcgagcattg 360
102 aacactgcac acggccatct gccagagag ctgtgaccac cacttccgct actagctagc 420
103 cgc 423

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